

# Introducción a la pan-genómica microbiana

IIIntroducción a la filoinformática – pan-genómica y filogenómica microbiana,  
TIB2025, 4-8 agosto, 2025 CCG-UNAM, Cuernavaca, Mor. México  
<https://github.com/vinuesa/TIB-filoinfo>

## Microbial genome evolution - the pan-genome

Pablo Vinuesa  
Centro de Ciencias Genómicas – UNAM  
vinuesa @ ccg.unam.mx  
<http://www.ccg.unam.mx/~vinuesa/>  
 @pvinmex

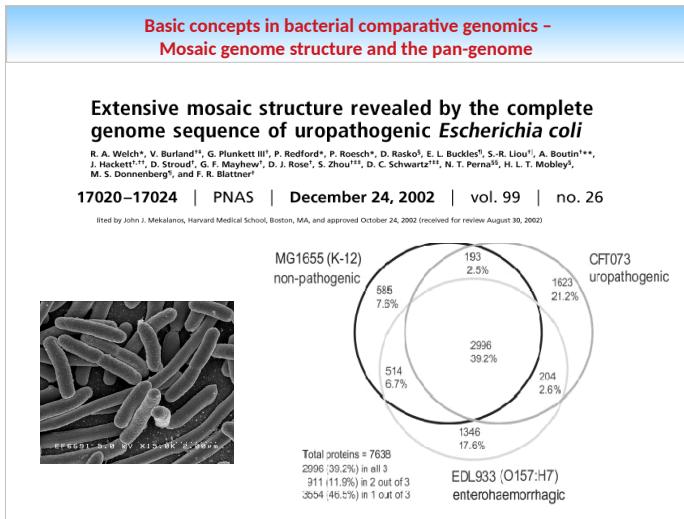
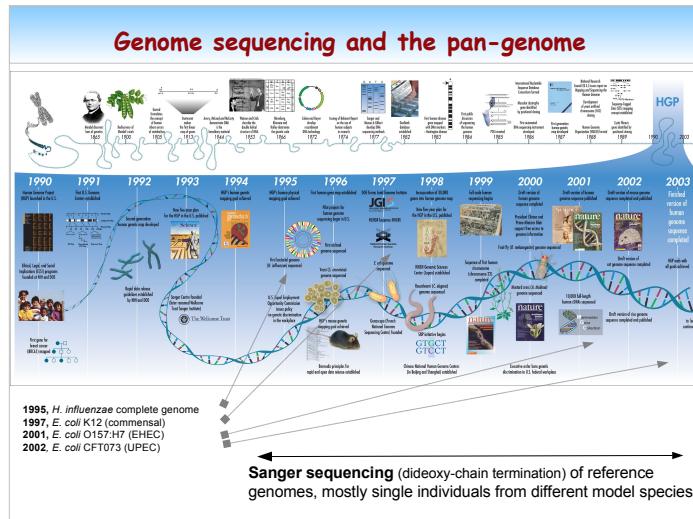
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NNB & CCG-UNAM, 4-8 agosto 2025  
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## Genome evolution and the pan-genome

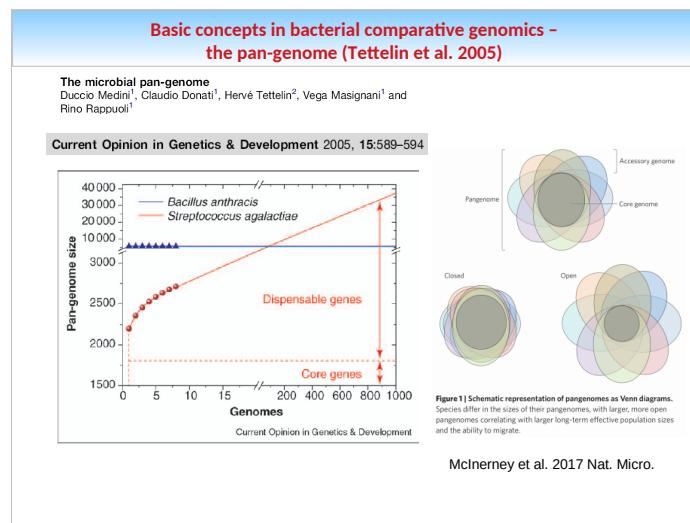
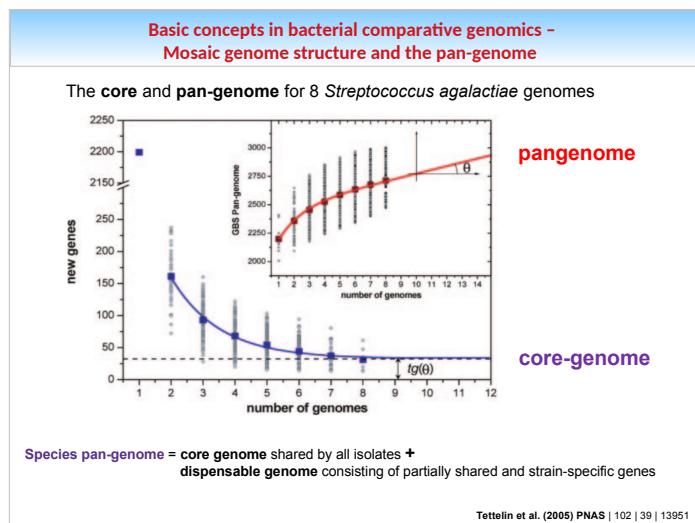
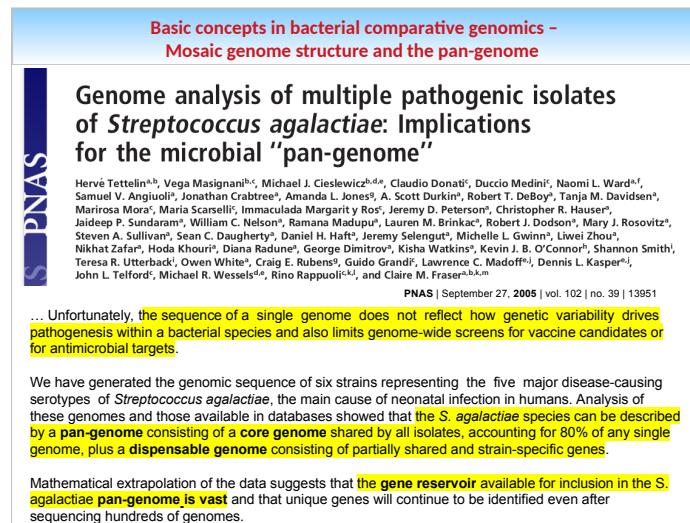
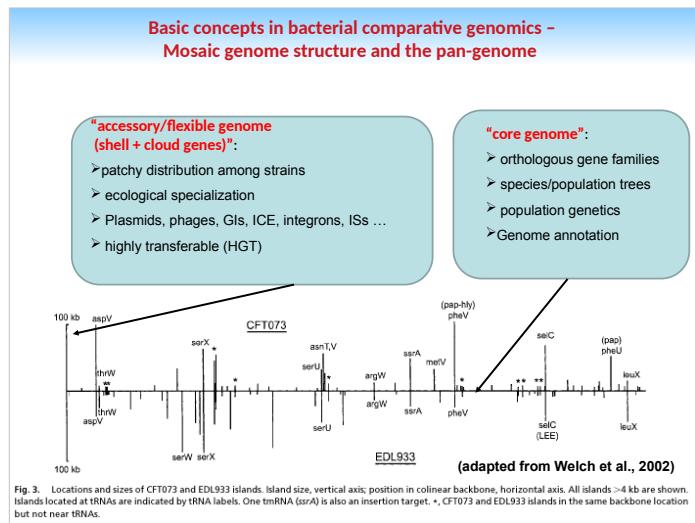
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1. Basic concepts in bacterial comparative genomics – defining the pan-genome
  - genome mosaicism and the pan-genome
  - Structure of the pan-genome: the core and accessory/flexible (shell and cloud) genomes
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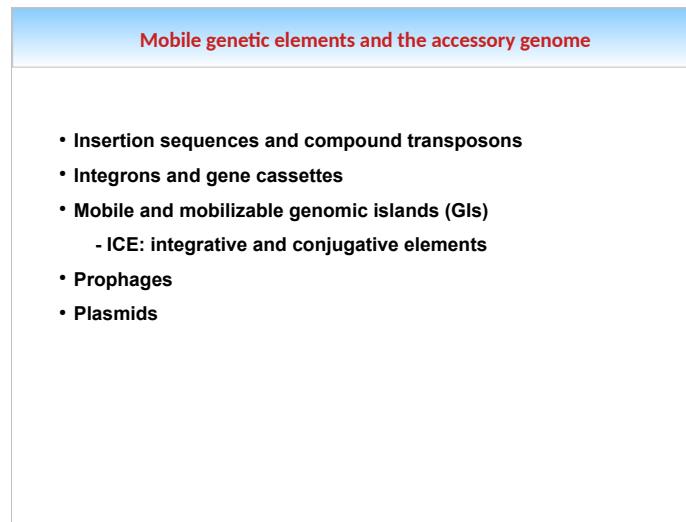
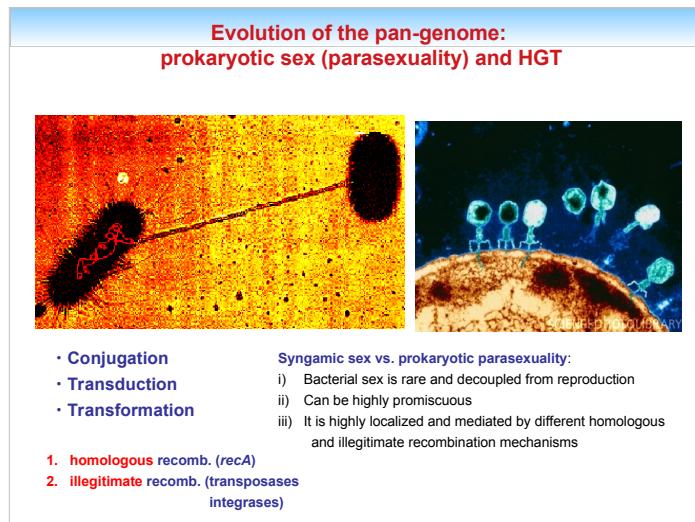
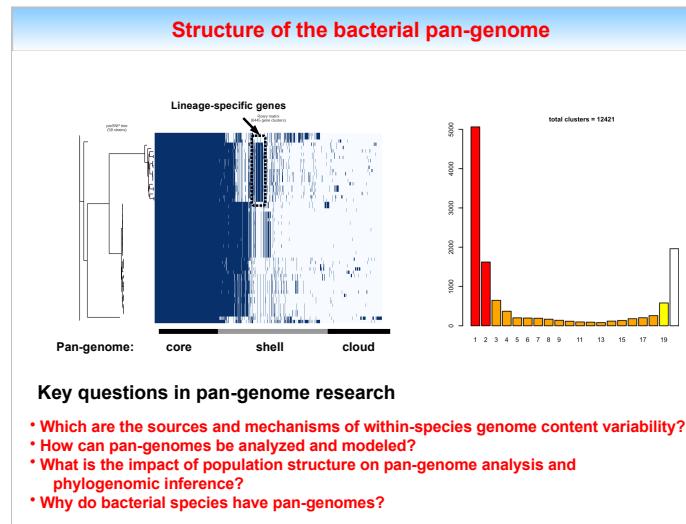
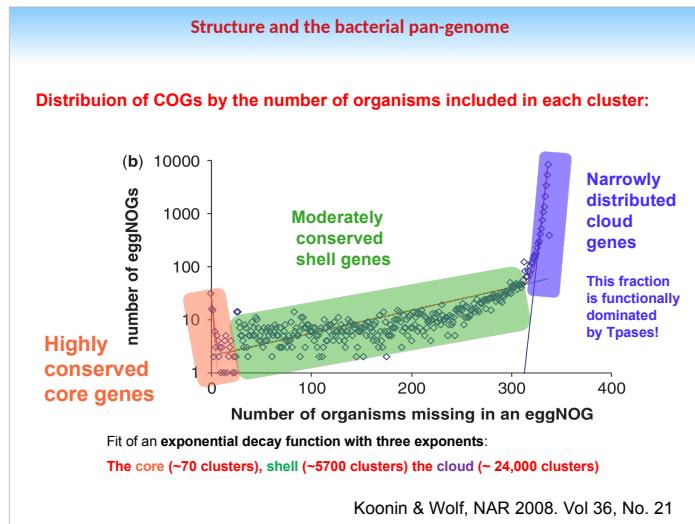
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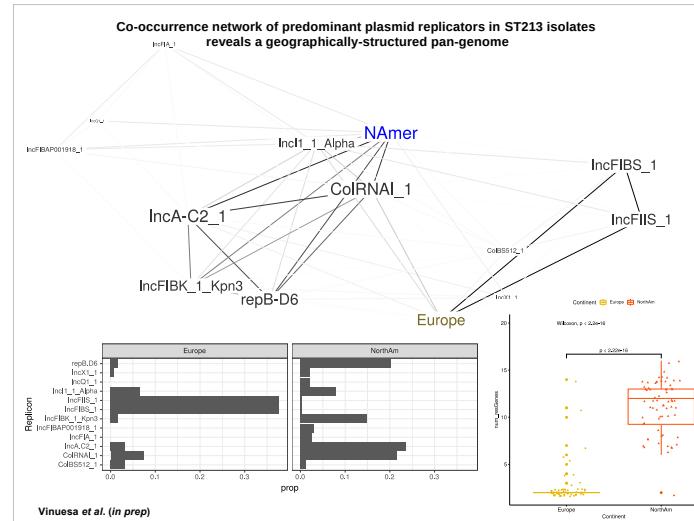
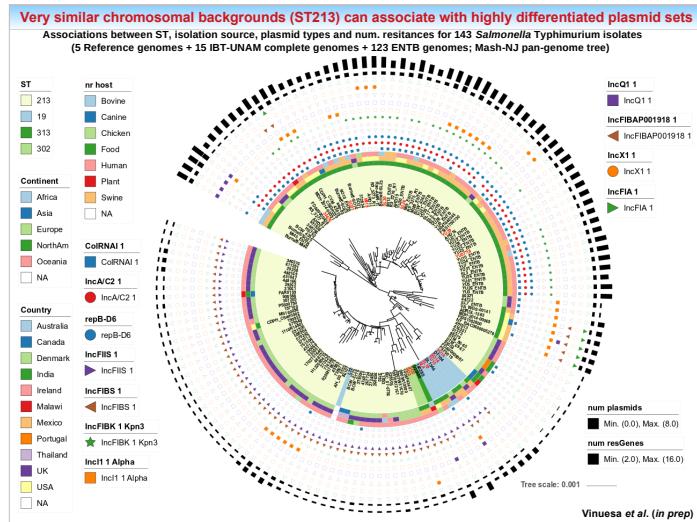
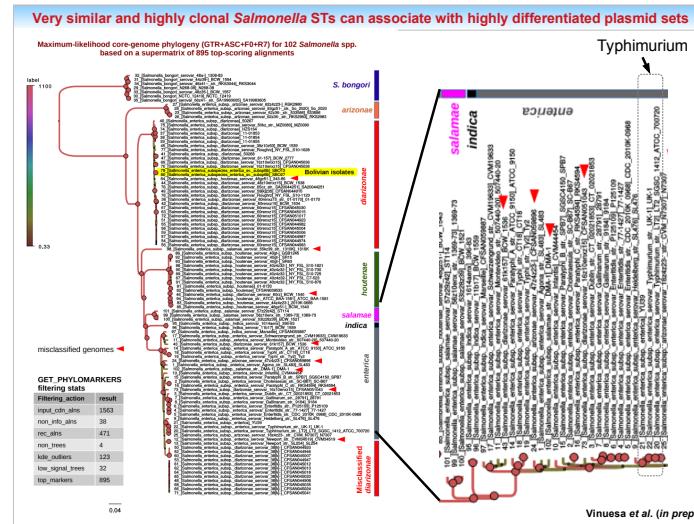
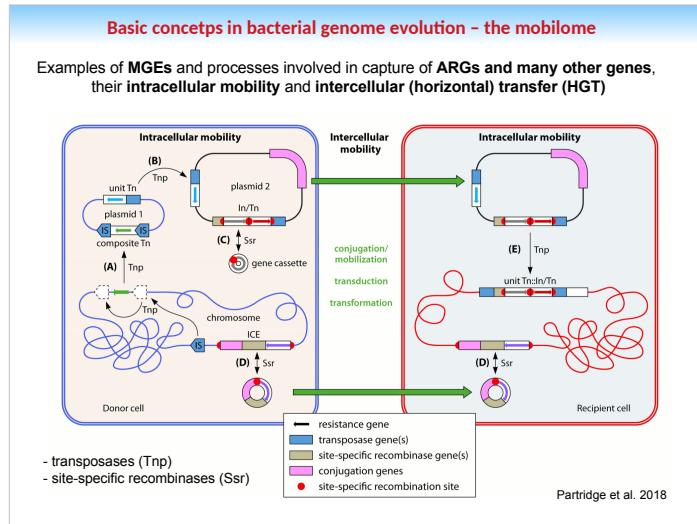
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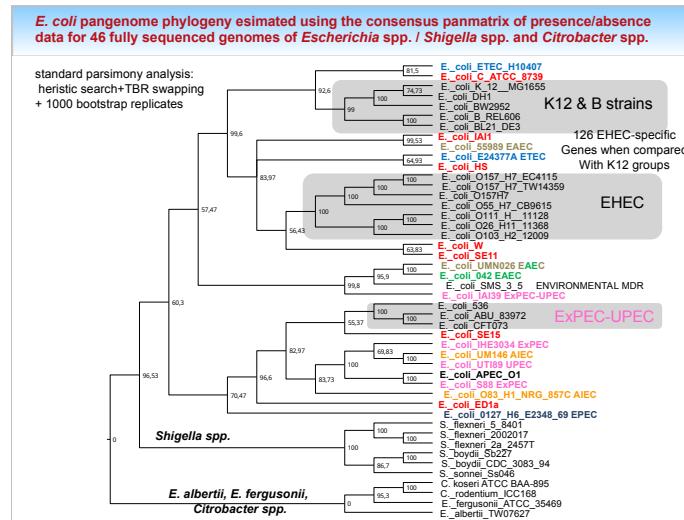
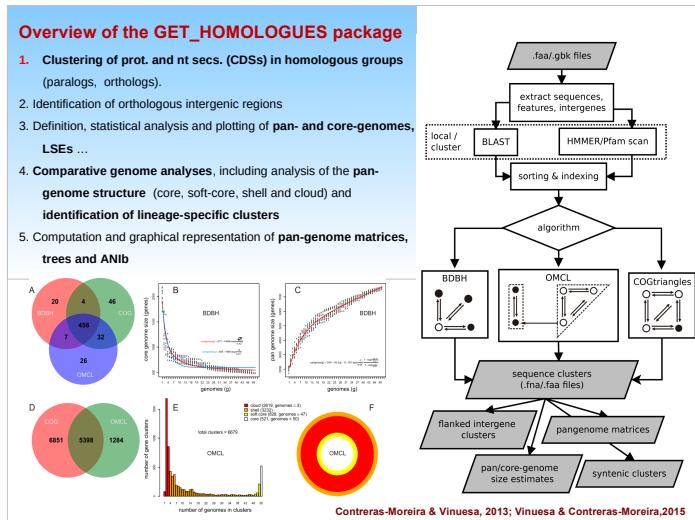
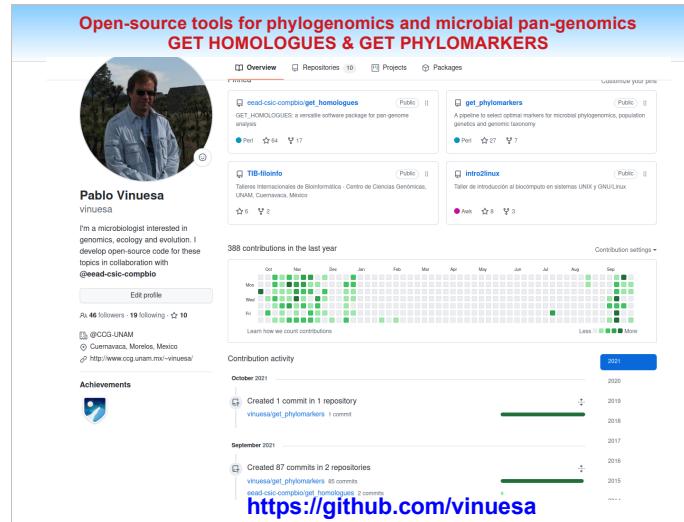
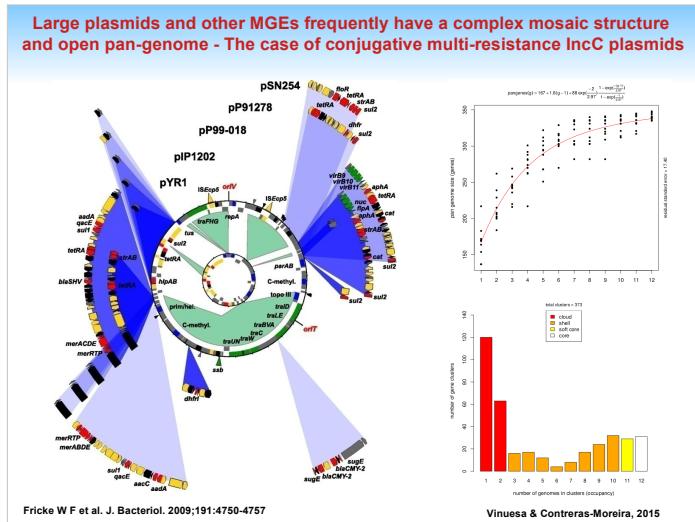
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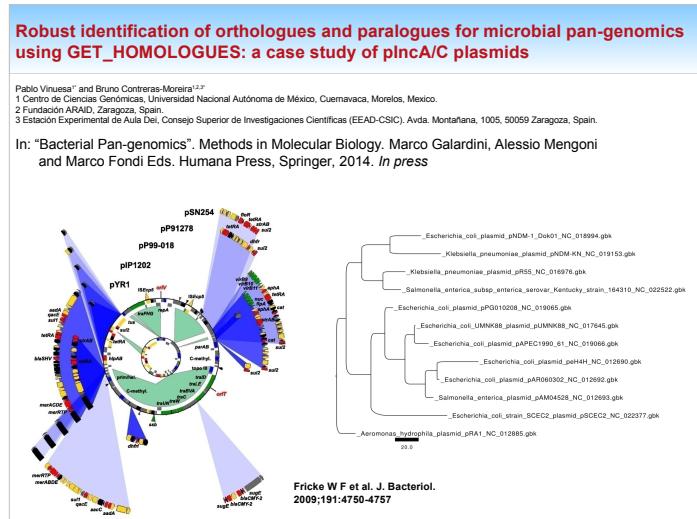
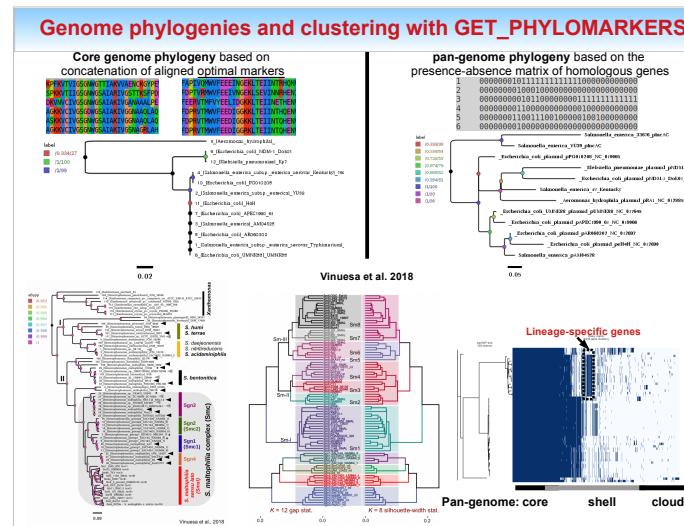
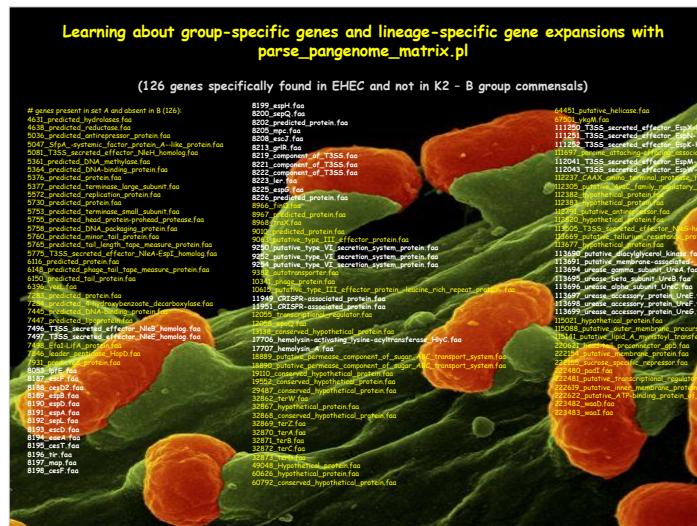
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<https://www.ccg.unam.mx/~vinuesa/>

## The GET\_HOMOLOGUES + GET\_PHYLOMARKERS tutorials

- [https://github.com/vinuesa/get\\_phylomarkers/](https://github.com/vinuesa/get_phylomarkers/)

#### **Analyses to be performed in an upcoming practical session**

## A pangenomic analysis of plncA/C plasmids using GET\_HOMOLOGUES

- Defining a robust core- and pan-genome of *plnC/A* plasmids
  - Exploring the gene space of *plnC/A* plasmids: core, shell, cloud
  - Pan-genome trees vs. core genome trees (supermatrices)
  - Identifying lineage-specific genes in NDM-1 producing plasmids

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Installing and running GET\_HOMOLOGUES through bioconda BIOCONDA

BIOCONDA®  
Navigation  
FAOs  
Contributing to Bioconda  
Developer Docs  
Tutorials

## Bioconda: sustainable and comprehensive software distribution for the life sciences

Björn Grüning, Ryan Dale, Andreas Sjödin, Brad A. Chapman, Jillian Rowe, Christopher H. Tomkins-Tinch, Renan Valieris, Johannes Köster & The Bioconda Team

Nature Methods 15, 475–476 (2018) | [Cite this article](#)

13k Accesses | 458 Citations | 231 Altmetric | [Metrics](#)

```
$ conda activate bioconda
$ conda create -n get_homologues -c conda-forge -c bioconda get_homologues
$ conda activate get_homologues
```

Installing and running GET\_HOMOLOGUES + GET\_PHYLOMARKERS is very easy launching ready-to-use Docker containers

bioconda/get\_homologues

13 million+ Docker Pull Command

Owner: csicunam

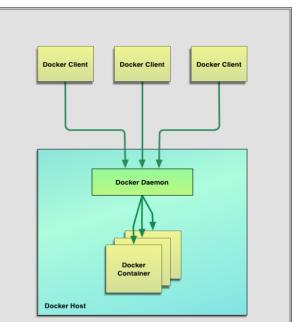
vinuesa/get\_phylomarkers

7 million+ Docker Pull Command

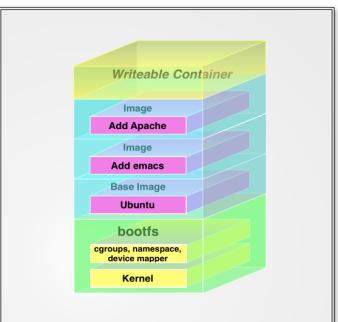
Owner: vinuesa

Installing and running GET\_HOMOLOGUES + GET\_PHYLOMARKERS is very easy launching ready-to-use Docker containers

General Docker architecture: running Docker containers via a Docker client to communicate with containers via the Docker Daemon



A Docker image is made up of filesystems layered over each other. At the base is a boot filesystem, **boots**, which resembles the typical Linux/Unix boot filesystem. Docker uses a **union mount** to add more read-only filesystems onto the root filesystem, which appear to be one filesystem.



Basic Docker commands and use of containers

```
## To avoid permission errors (and the use of sudo), add your user to the docker group
# https://docs.docker.com/install/linux/linux-postinstall/
sudo groupadd docker
sudo usermod -A $USER docker

# 1. Get general docker info and print help
$ docker info
$ docker --help
$ docker run --help

# 2. List available docker images on your system
$ docker image ls

# 3. List running containers
$ docker container ls

# 4. Stop a container
$ docker container stop CONTAINER-ID

# 5. Pull a Docker image from the registry
$ docker pull csicunam/get_homologues:latest

# 6. Launch an image, using a mount-bind of a user directory on the Docker container
$ docker run --rm -it -v $HOME/get_homPhy:/home/you/get_homPhy \
  csicunam/get_homologues:latest /bin/bash

# The last command uses options --rm to remove the container after exiting and sets an
# interactive session calling a pseudo tty (-t), mounting a host directory on the
# container (-v ...), accessible for wr from both, and launching a bash shell (/bin/bash)
```